

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/569,022  
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IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/569,022

DATE: 03/07/2006

TIME: 10:10:39

Input Set : E:\Final Sequence list-13173-00025-US.txt  
 Output Set: N:\CRF4\03072006\J569022.raw

3 <110> APPLICANT: Flachmann, Ralf  
 4 Schopfer, Christel Renate  
 5 Herbers, Karin  
 6 Kunze, Irene  
 7 Sauer, Matt  
 8 Klebsattel, Martin  
 9 Luck, Thomas  
 10 Voeste, Dirk  
 11 Pfeiffer, Angelika-Maria  
 13 <120> TITLE OF INVENTION: Method for producing ketocarotenoids in genetically modified,  
 14 non-human organisms  
 16 <130> FILE REFERENCE: 13173-00025-US  
 C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/569,022  
 C--> 18 <141> CURRENT FILING DATE: 2006-02-17  
 18 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/008623  
 19 <151> PRIOR FILING DATE: 2004-07-31  
 21 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09102  
 22 <151> PRIOR FILING DATE: 2003-08-18  
 24 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09107  
 25 <151> PRIOR FILING DATE: 2003-08-18  
 27 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09105  
 28 <151> PRIOR FILING DATE: 2003-08-18  
 30 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09106  
 31 <151> PRIOR FILING DATE: 2003-08-18  
 33 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09109  
 34 <151> PRIOR FILING DATE: 2003-08-18  
 36 <150> PRIOR APPLICATION NUMBER: PCT/EP03/09101  
 37 <151> PRIOR FILING DATE: 2003-08-18  
 39 <150> PRIOR APPLICATION NUMBER: DE 102004007622.7  
 40 <151> PRIOR FILING DATE: 2004-02-17  
 42 <160> NUMBER OF SEQ ID NOS: 137  
 44 <170> SOFTWARE: PatentIn version 3.3  
 48 <210> SEQ ID NO: 1  
 49 <211> LENGTH: 1666  
 50 <212> TYPE: DNA  
 51 <213> ORGANISM: Lycopersicon esculentum  
 53 <220> FEATURE:  
 54 <221> NAME/KEY: CDS  
 55 <222> LOCATION: (1)..(1494)  
 58 <400> SEQUENCE: 1  
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 60 Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Ser Ser Pro  
 61 1 5 10 15

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63 aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc	96
64 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro	
65 20 25 30	
67 acc acc aaa aaa tca aga aaa tgt ctt ctt aga aac aaa agt agt	144
68 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser	
69 35 40 45	
71 aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag	192
72 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu	
73 50 55 60	
75 tct tta gat gtt aac atc tca tgg gtt gat cct aat tcg aat cgg gct	240
76 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala	
77 65 70 75 80	
79 caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta	288
80 Gln Phe Asp Val Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu	
81 85 90 95	
83 gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct	336
84 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro	
85 100 105 110	
87 tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag	384
88 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu	
89 115 120 125	
91 ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg	432
92 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met	
93 130 135 140	
95 act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca	480
96 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro	
97 145 150 155 160	
99 tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt	528
100 Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Asn Ser	
101 165 170 175	
103 tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg	576
104 Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val	
105 180 185 190	
107 gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag	624
108 Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys	
109 195 200 205	
111 ata aga ggt agt ttg gtt gtg gat gca agt ggt ttt gct agt gat tt	672
112 Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe	
113 210 215 220	
115 ata gag tat gac agg cca aga aac cat ggt tat caa att gct cat ggg	720
116 Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly	
117 225 230 235 240	
119 gtt tta gta gaa gtt gat aat cat cca ttt gat ttg gat aaa atg gtg	768
120 Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val	
121 245 250 255	
123 ctt atg gat tgg agg gat tct cat ttg ggt aat gag cca tat tta agg	816
124 Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg	
125 260 265 270	
127 gtg aat aat gct aaa gaa cca aca ttc ttg tat gca atg cca ttt gat	864

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197 <213> ORGANISM: Lycopersicon esculentum  
 200 <400> SEQUENCE: 2  
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 203 1 5 10 15  
 206 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro  
 207 20 25 30  
 210 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser  
 211 35 40 45  
 214 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu  
 215 50 55 60  
 218 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala  
 219 65 70 75 80  
 222 Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu  
 223 85 90 95  
 226 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro  
 227 100 105 110  
 230 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu  
 231 115 120 125  
 234 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met  
 235 130 135 140  
 238 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro  
 239 145 150 155 160  
 242 Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Asn Ser  
 243 165 170 175  
 246 Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val  
 247 180 185 190  
 250 Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys  
 251 195 200 205  
 254 Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe  
 255 210 215 220  
 258 Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly  
 259 225 230 235 240  
 262 Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val  
 263 245 250 255  
 266 Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg  
 267 260 265 270  
 270 Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp  
 271 275 280 285  
 274 Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val  
 275 290 295 300  
 278 Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His  
 279 305 310 315 320  
 282 Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile  
 283 325 330 335  
 286 Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile  
 287 340 345 350  
 290 Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala  
 291 355 360 365  
 294 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly

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298	Leu	Gly	Ser	Thr	Arg	Met	Ile	Arg	Gly	Ser	Gln	Leu	Tyr	His	Arg	Val		
299	385					390			395						400			
302	Trp	Asn	Gly	Leu	Trp	Pro	Leu	Asp	Arg	Arg	Cys	Val	Arg	Glu	Cys	Tyr		
303						405			410						415			
306	Ser	Phe	Gly	Met	Glu	Thr	Leu	Leu	Lys	Leu	Asp	Leu	Lys	Gly	Thr	Arg		
307						420			425						430			
310	Arg	Leu	Phe	Asp	Ala	Phe	Phe	Asp	Leu	Asp	Pro	Lys	Tyr	Trp	Gln	Gly		
311						435			440						445			
314	Phe	Leu	Ser	Ser	Arg	Leu	Ser	Val	Lys	Glu	Leu	Gly	Leu	Leu	Ser	Leu		
315						450			455						460			
318	Cys	Leu	Phe	Gly	His	Gly	Ser	Asn	Met	Thr	Arg	Leu	Asp	Ile	Val	Thr		
319						465			470						475			
322	Lys	Cys	Pro	Leu	Pro	Leu	Val	Arg	Leu	Ile	Gly	Asn	Leu	Ala	Ile	Glu		
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336	<220>	FEATURE:																
337	<221>	NAME/KEY:	CDS															
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345	aataataaaag	agctcaagcg	tttgtgcgcc	tcgacgtggc	cagtctgcac	tgcccttgaac											120	
347	ccgcgcgtct	ccgcgcgcac	tgactgcccatt	agcacagacta	gacgaa	atgc	cag	cta	gca								177	
348															Met	Gln	Leu	Ala
349															1			
351	gcg	aca	gtt	atg	ttg	gag	cag	ctt	acc	gga	agc	gct	gag	gca	ctc	aag		
352	Ala	Thr	Val	Met	Leu	Glu	Gln	Leu	Thr	Gly	Ser	Ala	Glu	Ala	Leu	Lys		
353	5				10				15							20		
355	gag	aag	gag	aag	gag	gtt	gca	ggc	agc	tct	gac	gtg	ttg	cgt	aca	tgg		
356	Glu	Lys	Glu	Lys	Glu	Val	Ala	Gly	Ser	Ser	Asp	Val	Leu	Arg	Thr	Trp		
357						25			30							35		
359	gcg	acc	cag	tac	tcg	ctt	ccg	tca	gaa	gag	tca	gac	gcg	gcc	cgc	ccg		
360	Ala	Thr	Gln	Tyr	Ser	Leu	Pro	Ser	Glu	Glu	Ser	Asp	Ala	Ala	Arg	Pro		
361						40			45							50		
363	gga	ctg	aag	aat	gcc	tac	aag	cca	cca	cct	tcc	gac	aca	aag	ggc	atc		
364	Gly	Leu	Lys	Asn	Ala	Tyr	Lys	Pro	Pro	Pro	Ser	Asp	Thr	Lys	Gly	Ile		
365						55			60							65		
367	aca	atg	gct	cta	cgt	gtc	atc	ggc	tcc	tgg	gcc	gca	gtg	ttc	ctc	cac		
368	Thr	Met	Ala	Leu	Arg	Val	Ile	Gly	Ser	Trp	Ala	Ala	Val	Phe	Leu	His		
369						70			75							80		
371	gcc	att	ttt	caa	atc	aag	ctt	ccg	acc	tcc	ttg	gac	cag	ctg	cac	tgg		
372	Ala	Ile	Phe	Gln	Ile	Lys	Leu	Pro	Thr	Ser	Leu	Asp	Gln	Leu	His	Trp		
373						85			90							95		100
375	ctg	ccc	gtg	tca	gat	gcc	aca	gct	cag	ctg	gtt	agc	ggc	acg	agc	agc		
376	Leu	Pro	Val	Ser	Asp	Ala	Thr	Ala	Gln	Leu	Val	Ser	Gly	Thr	Ser	Ser		

**VERIFICATION SUMMARY**

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Input Set : E:\Final Sequence list-13173-00025-US.txt  
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L:18 M:270 C: Current Application Number differs, Replaced Current Application No  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date